Table 2: Peptide Binding to Bcl-2/iso1

Sequence	SEQ. ID NO:	K_d (nM)
NLWAAQRYGRELRRMSDEFVDSFKK	**20**	14
ALWAAQRYGRELRRMSDEFVDSFKK	**21**	211
NAWAAQRYGRELRRMSDEFVDSFKK	**22**	75
NLAAAQRYGRELRRMSDEFVDSFKK	**23**	39
AAAAAQRYGRELRRMSDEFVDSFKK	**17**	74
NLWGAQRYGRELRRMSDEFVDSFKK	**24**	159
NLWAGQRYGRELRRMSDEFVDSFKK	**25**	105
NLWAAQRYGRELRRMSDEFVDAFKK	**26**	26
NLWAAQRYGRELRRMSDEFVDSAKK	**27**	397
NLWAAQRYGRELRRMSDEFVDSFAK	**28**	123
NLWAAQRYGRELRRMSDEFVDSFKA	**29**	22
GGGAAQRYGRELRRMSDEFVDSFKK	**30**	63
NLPAAQRYGRELRRMSDEFVDSFKK	**31**	54
NLWAAQRYARELRRMSDEFVAAFKK	**32**	186
NLWAAQRYGREARRMSDEFVDSFKK	**33**	7483
NLWAAQRYGRELRRMSAEFVDSFKK	**34**	762
QRYGRELRRMSDEFVDSFKK	**35**	711
NLWAAQRYGRELRRMSDEFVD	**36**	2326

Table 3: Peptide Binding to Bcl-2/iso2

Sequence	SEQ. ID NO:	K_d (nM)
NLWAAQRYGRELRRMSDEFVDSFKK	**20**	8
GQVGRQLAIIGDDINR	**37**	

1600

As Tables 2 and 3 show, the mutant proteins of the invention can be used for identifying compounds which bind tightly to a Bcl-2 family member.

EXAMPLE 3: Structure Determination of Bcl-2/iso1 and Bcl-2/iso2 by NMR

NMR Spectroscopy: The structures of soluble Bcl-2/iso1 and Bcl-2/iso2 were determined by NMR spectroscopy (see Figure 3). All NMR experiments were acquired at 298 K on a Bruker DRX500, DRX600 or DRX800 NMR spectrometer. Backbone ^{1}H, ^{13}C, and ^{15}N resonance assignments were achieved with [^{15}N,^{13}C,(75%)^{2}H] Bcl-2 using a suite of deuterium-decoupled, triple-resonance experiments (HNCA, HN(CO)CA, HN(CA)CB, HN(COCA)CB, HNCO and HN(CA)CO) (Yamazaki, T., Lee, W., Arrowsmith, C. H., Muhandiram, D. R. & Kay, L. E. (1994) *J. Am. Chem. Soc.* **116,** 11655-11666). The side-chain ^{1}H and ^{13}C NMR signals were assigned from HCCH-TOCSY experiments (Clore, G. M. & Gronenborn, A. M. (1994) *Methods Enzymol* **239,** 349-63), and stereospecific assignments of the valine and leucine methyl groups were obtained from an analysis of the ^{13}C-^{13}C coupling patterns observed for biosynthetically directed, fractionally ^{13}C-labeled Bcl-2 (Neri, D., Szyperski, T., Otting, G., Senn, H. & Wüthrich, K. (1989) *Biochemistry* **28,** 7510-7516). NOE distance restraints were obtained from three-dimensional ^{15}N- and ^{13}C-edited NOESY spectra (Fesik, S. W. & Zuiderweg, E. R. P. (1988) *J. Magn. Reson.* **78,** 588-593, Marion, D., Driscoll, P. C., Kay, L. E., Wingfield, P. T., Bax, A., Gronenborn, A. M. & Clore, G. M. (1989) *Biochemistry* **29,** 6150-6156) acquired with a mixing time of 80 ms. Slowly exchanging amide protons were identified in an ^{15}N-HSQC spectrum recorded immediately after exchanging the protein into a buffer prepared with D_2O. Residual dipolar couplings (HN-N and C'-C^{α}) were measured using undecoupled versions of the HNCO experiment on [^{15}N,^{13}C,(75%)^{2}H] Bcl-2 in the presence of 17 mg mL^{-1} Pf1 phage (Tjandra, N. (1999) *Structure* **7,** R205-R211, Hansen, M. R., Mueller, L. & Pardi, A. (1998)

Nature Struc. Biol. **5,** 1065-1074, Clore, G. M., Starich, M. R. & Gronenborn, A. M. (1998) *J. Am. Chem. Soc.* **120,** 1-571-10572).

Structure Calculations: Bcl-2 structures were calculated using a simulated annealing protocol (Brunger, A. T. (1992) *X-PLOR Version 3.1.* (Yale University Press, New Haven and London) with the program CNX (MSI, San Diego). A square-well potential (F_{NOE} = 50 kcal mol^{-1}) was employed to constrain NOE-derived distances. Based on the cross peak intensities, NOE-derived distance restraints were given upper bounds of 3.0, 4.0, 5.0, or 6.0 Å. Torsion angle restraints ϕ,ψ were generated from analysis of N, C', C^{α}, and H^{α} chemical shifts using the TALOS program (Cornilescu, G., Delaglio, F. & Bax, A. (1999) *J. Biomol. NMR* **13,** 289-302). A force constant of 200 kcal mol^{-1} rad^{-2} was applied to all torsional restraints. Explicit hydrogen bonds were included in α-helices only for residues observed to have slowly exchanging amide protons. The program PROCHECK was employed to analyze the geometric quality of the calculated structures in the ensemble (Laskowski, R. A., MacArthur, M. W., Moss, D. S. & Thornton, J. M. (1993) *J. Appl. Cryst.* **26,** 283-291).

The present invention is illustrated by way of the foregoing description and examples. The foregoing description is intended as a non-limiting illustration, since many variations will become apparent to those skilled in the art in view thereof. It is intended that all such variations within the scope and spirit of the appended claims be embraced thereby.

Changes can be made to the composition, operation and arrangement of the method of the present invention described herein without departing from the concept and scope of the invention as defined in the following claims.

Any references referred to herein are incorporated by reference.

SEQUENCE LISTING

<110> Fesik, Steven W.
Petros, Andrew M.
Yoon, Ho Sup
Nettescheim, David G.

<120> MUTANT BCL-2 PEPTIDES AND USES THEREOF

<130> 6752.US.01

<160> 37

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 16
<212> PRT
<213> Homo sapiens

<400> 1
Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu
1 5 10 15

<210> 2
<211> 166
<212> PRT
<213> Homo sapiens

<400> 2
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
20 25 30
Gly Asp Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu
35 40 45
Ser Glu Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser
50 55 60
Arg Arg Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu
65 70 75 80
Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu
85 90 95
Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe
100 105 110
Gly Gly Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu
115 120 125
Val Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu
130 135 140
His Thr Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu
145 150 155 160
Tyr Gly Pro Ser Met Arg
165

<210> 3

<211> 239
<212> PRT
<213> Homo sapiens

<400> 3
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
20 25 30
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
35 40 45
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
50 55 60
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65 70 75 80
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
85 90 95
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
100 105 110
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
115 120 125
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
130 135 140
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145 150 155 160
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
165 170 175
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
180 185 190
Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
195 200 205
Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
210 215 220
Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
225 230 235

<210> 4
<211> 239
<212> PRT
<213> Homo sapiens

<400> 4
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
20 25 30
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
35 40 45
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
50 55 60
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65 70 75 80
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
85 90 95
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
100 105 110
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly

```
        115                 120                 125
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
    130                 135                 140
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145                 150                 155                 160
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
                165                 170                 175
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
            180                 185                 190
Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
        195                 200                 205
Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
    210                 215                 220
Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
225                 230                 235


<210> 5
<211> 239
<212> PRT
<213> Homo sapiens

<400> 5
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1               5                  10                  15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
            20                  25                  30
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Phe
        35                  40                  45
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
    50                  55                  60
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
65                  70                  75                  80
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
                85                  90                  95
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
            100                 105                 110
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
        115                 120                 125
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
    130                 135                 140
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145                 150                 155                 160
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
                165                 170                 175
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
            180                 185                 190
Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
        195                 200                 205
Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
    210                 215                 220
Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
225                 230                 235


<210> 6
<211> 237
<212> PRT
```

<213> Homo sapiens

<400> 6

```
Met Ser Met Ala Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe
 1               5                  10                  15
Leu Ser Tyr Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser
            20                  25                  30
Asp Val Glu Glu Asn Arg Thr Glu Ala Pro Glu Glu Thr Glu Ser Glu
        35                  40                  45
Met Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala
    50                  55                  60
Asp Ser Pro Ala Val Asn Gly Ala Thr Gly His Ser Ser Ser Leu Asp
65                  70                  75                  80
Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu
                85                  90                  95
Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu
            100                 105                 110
Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu
        115                 120                 125
Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
    130                 135                 140
Val Ala Phe Phe Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp
145                 150                 155                 160
Lys Glu Met Gln Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr
                165                 170                 175
Tyr Leu Asn Asp His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp
            180                 185                 190
Asp Thr Phe Val Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg
        195                 200                 205
Lys Gly Gln Glu Arg Phe Asn Arg Trp Phe Leu Thr Gly Met Thr Val
    210                 215                 220
Ala Gly Val Val Leu Leu Gly Ser Leu Phe Ser Arg Lys
225                 230                 235
```

<210> 7
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
cactcaccat atggctcacg ctgggagaac ggggtacgac aac 43

<210> 8
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 8
gcgagctctc gagcttcaga gacagccagg agaaatcaaa cag 43

<210> 9

<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 9
gccccagaag ggactgaatc ggaggtggtc cacctggccc tccgccaa 48

<210> 10
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 10
ctcagtacgg ttctcttcca catcatctcc cgcatcccac tcgtagcc 48

<210> 11
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
cactcaccat atggctcacg ctgggagaac ggggtacgac aac 43

<210> 12
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 12
gcgaagctct cgagctatca atcaaacaga ggccgcatgc tggggccgta 50

<210> 13
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
gaggtggtcc acctgaccct ccgccaagcc g 31

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
cggcttggcg gagggtcagg tggaccacct c 31

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
gccgctaccg ccgcgacttc gccgag 26

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
ctcggcgaag tcgcggcggt agcggc 26

<210> 17
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 17
Ala Ala Ala Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
1 5 10 15
Asp Glu Phe Val Asp Ser Phe Lys Lys
20 25

<210> 18
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 18
Ala Ala Ala Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
1 5 10 15
Asp Glu Phe Val Asp Ser Lys Lys
20

```
<210> 19
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 19
Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser Asp Glu Phe
 1               5                  10                  15
Val Arg



<210> 20
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 20
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1               5                  10                  15
Asp Glu Phe Val Asp Ser Phe Lys Lys
            20                  25


<210> 21
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 21
Ala Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1               5                  10                  15
Asp Glu Phe Val Asp Ser Phe Lys Lys
            20                  25


<210> 22
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 22
Asn Ala Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1               5                  10                  15
Asp Glu Phe Val Asp Ser Phe Lys Lys
```

20 25

<210> 23
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 23
Asn Leu Ala Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
1 5 10 15
Asp Glu Phe Val Asp Ser Phe Lys Lys
20 25

<210> 24
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 24
Asn Leu Trp Gly Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
1 5 10 15
Asp Glu Phe Val Asp Ser Phe Lys Lys
20 25

<210> 25
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 25
Asn Leu Trp Ala Gly Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
1 5 10 15
Asp Glu Phe Val Asp Ser Phe Lys Lys
20 25

<210> 26
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 26
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser

```
 1               5                   10                  15
Asp Glu Phe Val Asp Ala Phe Lys Lys
            20                  25


<210> 27
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 27
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1               5                   10                  15
Asp Glu Phe Val Asp Ser Ala Lys Lys
            20                  25


<210> 28
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 28
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1               5                   10                  15
Asp Glu Phe Val Asp Ser Phe Ala Lys
            20                  25


<210> 29
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 29
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1               5                   10                  15
Asp Glu Phe Val Asp Ser Phe Lys Ala
            20                  25


<210> 30
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide
```

```
<400> 30
Gly Gly Gly Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1               5                  10                  15
Asp Glu Phe Val Asp Ser Phe Lys Lys
            20                  25


<210> 31
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 31
Asn Leu Pro Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1               5                  10                  15
Asp Glu Phe Val Asp Ser Phe Lys Lys
            20                  25


<210> 32
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 32
Asn Leu Trp Ala Ala Gln Arg Tyr Ala Arg Glu Leu Arg Arg Met Ser
 1               5                  10                  15
Asp Glu Phe Val Ala Ala Phe Lys Lys
            20                  25


<210> 33
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 33
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Ala Arg Arg Met Ser
 1               5                  10                  15
Asp Glu Phe Val Asp Ser Phe Lys Lys
            20                  25


<210> 34
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
```

<223> peptide

<400> 34
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1 5 10 15
Ala Glu Phe Val Asp Ser Phe Lys Lys
 20 25

<210> 35
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 35
Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser Asp Glu Phe Val Asp
 1 5 10 15
Ser Phe Lys Lys
 20

<210> 36
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 36
Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu Arg Arg Met Ser
 1 5 10 15
Asp Glu Phe Val Asp
 20

<210> 37
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 37
Gly Gln Val Gly Arg Gln Leu Ala Ile Ile Gly Asp Asp Ile Asn Arg
 1 5 10 15